

SEQUENCE LISTING

<110> Vinkemeier, Uwe  
Darnell Jr., James E.

<120> PURIFIED STAT PROTEINS AND METHODS OF PURIFYING THEREOF

<130> 600-1-182 N

<140> 08/951,130  
<141> 1997-10-15

<150> 60/028,176  
<151> 1996-10-15

<160> 16

<170> PatentIn Ver. 2.0

<210> 1  
<211> 750  
<212> PRT  
<213> Homo sapiens

<400> 1  
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20 25 30  
Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn  
35 40 45  
Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu  
50 55 60  
Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln  
65 70 75 80  
His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu  
85 90 95  
Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu  
100 105 110  
Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly  
115 120 125

Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser  
130 135 140

Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile  
145 150 155 160

Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr  
165 170 175

Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln  
180 185 190

Lys Gln Glu Gln Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn  
195 200 205

Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr  
210 215 220 -

Glu Leu Thr Gln Asn Ala Leu Asn Asp Glu Leu Val Glu Trp Lys  
225 230 235 240

Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu  
245 250 255

Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln  
260 265 270

Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr  
275 280 285

Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg  
290 295 300

Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu  
305 310 315 320

Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys  
325 330 335

Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln  
340 345 350

Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val  
355 360 365

Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly  
370 375 380

Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu  
385 390 395 400

Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly  
405 410 415

Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser  
420 425 430

Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu  
435 440 445

Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu  
450 455 460

Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu  
465 470 475 - 480

Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala  
485 490 495

Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg  
500 505 510

Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly  
515 520 525

Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys  
530 535 540

Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser  
545 550 555 560

Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly  
565 570 575

Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys  
580 585 590

Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg  
595 600 605

Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly  
610 615 620

Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser  
625 630 635 640

Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala  
645 650 655

Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp  
660 665 670

Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro  
675 680 685

Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr  
690 695 700

Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr  
705 710 715 720

Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Val Ser Arg  
725 730 - 735

Ile Val Gly Ser Val Glu Phe Asp Ser Met Met Asn Thr Val  
740 745 750

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<211> 712

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu  
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Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln  
20 25 30

Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn  
35 40 45

Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu  
50 55 60

Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln  
65 70 75 80

His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu  
85 90 95

Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu

100

105

110

Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly  
115 120 125

Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser  
130 135 140

Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile  
145 150 155 160

Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr  
165 170 175

Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln  
180 185 190

Lys Gln Glu Gln Leu Leu Lys Lys Met Tyr Leu Met-Leu Asp Asn  
195 200 205

Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr  
210 215 220

Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys  
225 230 235 240

Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu  
245 250 255

Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln  
260 265 270

Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr  
275 280 285

Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg  
290 295 300

Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu  
305 310 315 320

Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys  
325 330 335

Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln  
340 345 350

Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val

355

360

365

Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly  
370 375 380

Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu  
385 390 395 400

Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly  
405 410 415

Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser  
420 425 430

Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu  
435 440 445

Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu  
450 455 460

Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu  
465 470 475 480

Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala  
485 490 495

Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg  
500 505 510

Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly  
515 520 525

Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys  
530 535 540

Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser  
545 550 555 560

Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly  
565 570 575

Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys  
580 585 590

Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg  
595 600 605

Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly

610

615

620

Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser  
625 630 635 640

Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala  
645 650 655

Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp  
660 665 670

Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro  
675 680 685

Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr  
690 695 700

Glu Leu Ile Ser Val Ser Glu Val  
705 710

<210> 3

<211> 582

<212> PRT

<213> Homo sapiens

<400> 3

Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser Lys Val Arg  
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Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile Lys Ser Leu  
20 25 30

Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr Leu Gln Asn  
35 40 45

Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln Lys Gln Glu  
50 55 60

Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn Lys Arg Lys  
65 70 75 80

Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr Glu Leu Thr  
85 90 95

Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys Arg Arg Gln  
100 105 110

Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu Asp Gln Leu  
115 120 125

Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln Val Arg Gln  
130 135 140

Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr Tyr Glu His  
145 150 155 160

Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg Thr Phe Ser  
165 170 175

Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu Arg Gln Pro  
180 185 190

Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys Thr Gly Val  
195 200 205

Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln Glu Leu Asn  
210 215 220

Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val Asn Glu Arg  
225 230 235 240

Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly Thr His Thr  
245 250 255

Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu Ala Ala Glu  
260 265 270

Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly Thr Arg Thr  
275 280 285

Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser Leu Ser Phe  
290 295 300

Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu Glu Thr Thr  
305 310 315 320

Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu Pro Ser Gly  
325 330 335

Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu Pro Arg Asn  
340 345 350

Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala Gln Leu Ser  
355 360 365

Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg Gly Leu Asn  
370 375 380

Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly Pro Asn Ala  
385 390 395 400

Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys Glu Asn Ile  
405 410 415

Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser Ile Leu Glu  
420 425 430

Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly Cys Ile Met  
435 440 445

Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys Asp Gln Gln  
450 455 460

Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg Glu Gly Ala  
465 470 475 480

Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly Glu Pro Asp  
485 490 495

Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser Ala Val Thr  
500 505 510

Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala Glu Asn Ile  
515 520 525

Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp Lys Asp His  
530 535 540

Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro Glu Pro Met  
545 550 555 560

Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr Glu Leu Ile  
565 570 575

Ser Val Ser Glu Val His  
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<211> 131  
<212> PRT  
<213> Homo sapiens

<400> 4

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu  
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Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln  
20 25 30

Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn  
35 40 45

Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu  
50 55 60

Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln  
65 70 75 80

His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu  
85 90 95

Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu  
100 105 110

Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly  
115 120 125

Asn Ile Gln

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<210> 5

<211> 1746

<212> DNA

<213> Homo sapiens

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ttcaaatgca aaaccttgca gaacagagaa cacgagacca atggtgtggc aaagagtgtat 180  
cagaaacaag aacagctgtt actcaagaag atgtatcaa tgcttgacaa taagagaaag 240  
gaagtagttc acaaaaataat agagttgctg aatgtcactg aacttaccca gaatgccctg 300  
attaatgtatg aactagtggc gtggaaagccg agacagcaga ggcgcctgtat tggggggccg 360  
cccaatgctt gcttggatca gctgcagaac tggttcacta tagttgcgg aagtctgcag 420  
caagttcgac agcagcttaa aaagttggag gaattggac agaaatacac ctacgaacat 480  
gaccctatca caaaaaacaa acaagtgtt tgggaccgca ctttcagtct tttccagcag 540  
ctcattcaga gctcgttgt ggtggaaaga cagccctgca tgccaaacgca ccctcagagg 600  
ccgctggctc tgaagacagg ggtccagttc actgtgaagt tgagactgtt ggtgaaattg 660  
caagagctga attataattt gaaagtcaaa gtcttatttg ataaagatgt gaatgagaga 720  
aatacgtaa aaggat tag gaagttcaac atttggcga cgcacacaaa agtgcgtt 780

atggaggagt ccaccaatgg cagtctggcg gctgaatttc ggcacctgca attgaaagaa 840  
cagaaaaatg ctggcaccag aacgaatgag ggtcctctca tcgttactga agagcttcac 900  
tcccttagtt ttgaaaccca attgtgccag cctgggttg taattgaccc cgagacgacc 960  
tctctgcccg ttgtgggtat ctccaaacgtc agccagctcc cgagcgggtg ggcctccatc 1020  
ctttggtaca acatgctggt ggcggAACCC aggaatctgt ccttcttctt gactccacca 1080  
tgtgcacat gggctcagct ttcagaagtg ctgagttggc agtttcttc tgtcaccaaa 1140  
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tttcccttctt ggcttggat tgaaagcatc ctagaactca ttaaaaaaca cctgctccct 1320  
ctctggaatg atgggtgcatt catgggcttc atcagcaagg agcgagagcg tgccctgtt 1380  
aaggaccagc agccggggac cttcctgctg cggttcagtg agagctcccg ggaagggggcc 1440  
atcacattca catgggtgga gcggtcccag aacggaggcg aacctgactt ccatgcgggt 1500  
gaaccctaca cgaagaaaga actttctgct gttaactttcc ctgacatcat tcgcaattac 1560  
aaagtcatgg ctgctgagaa tattcctgag aatcccctga agtatactgta tccaaatatt 1620  
gacaaagacc atgcctttgg aaagtattac tccaggccaa aggaagcacc agagccaaatg 1680  
gaacttgcgt gccctaaagg aactggatat atcaagactg agttgatttc tgtgtctgaa 1740  
gttcac 1746

<210> 6  
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<212> DNA  
<213> Homo sapiens

<400> 6  
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ctttatgatg acagtttcc catggaaatc agacagtacc tggcacagtg gttagaaaaag 120  
caagactggg agcacgctgc caatgatgtt tcatttgcca ccatccgttt tcatgaccc 180  
ctgtcacagc tggatgatca atatagtcgc ttttcttgg agaataactt cttgctacag 240  
cataacataa ggaaaagcaa gcgtaatctt caggataatt ttcaggaaga cccaatccag 300  
atgtctatga tcatttacag ctgtctgaaag gaagaaagga aaattctgga aaacgcccag 360  
agatttaatc aggctcagtc gggaaatatt cag 393

<210> 7  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 7  
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<210> 8  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 8

cggatcctat tagtgaactt cagacacaga aatc

34

<210> 9

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 9

gtattcccggt caatgca

17

<210> 10

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 10

gtattccctgt aagatct

17

<210> 11

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 11

gatttcccggt aaatcat

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<210> 12

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 12

gttgttccgg gaaaagg

17

<210> 13  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 13  
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40

<210> 14  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

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agtcaagtcc cgtcaatgag ttcccgtaa tgca

34

<210> 15  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

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43

<210> 16  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 16  
agtcatatcc cgtcaatgca tcagttgacg ggaaaagtatg

40